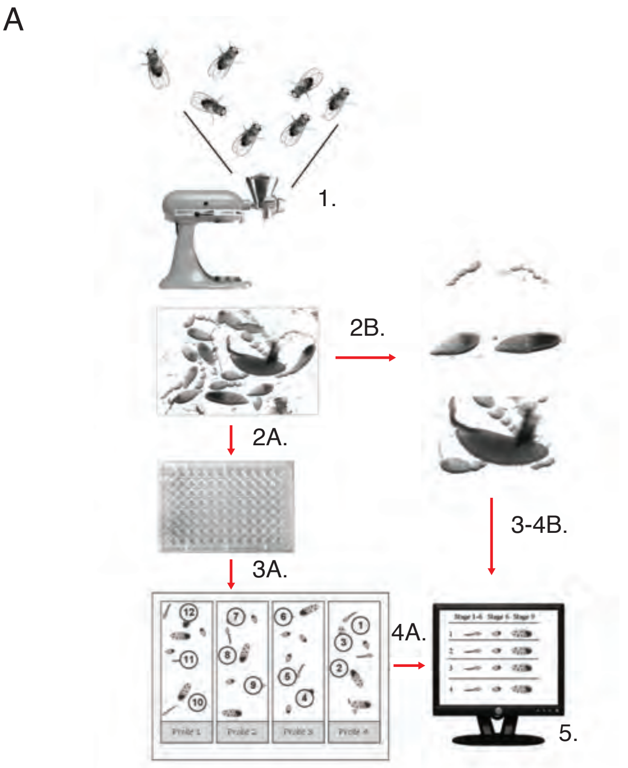
Figure S1



1. Mass isolation of egg-chambers from whole flies.

2A. 96-well fluorescent in situ hybridization.

2B. Manual selection of stage specific egg-chambers.

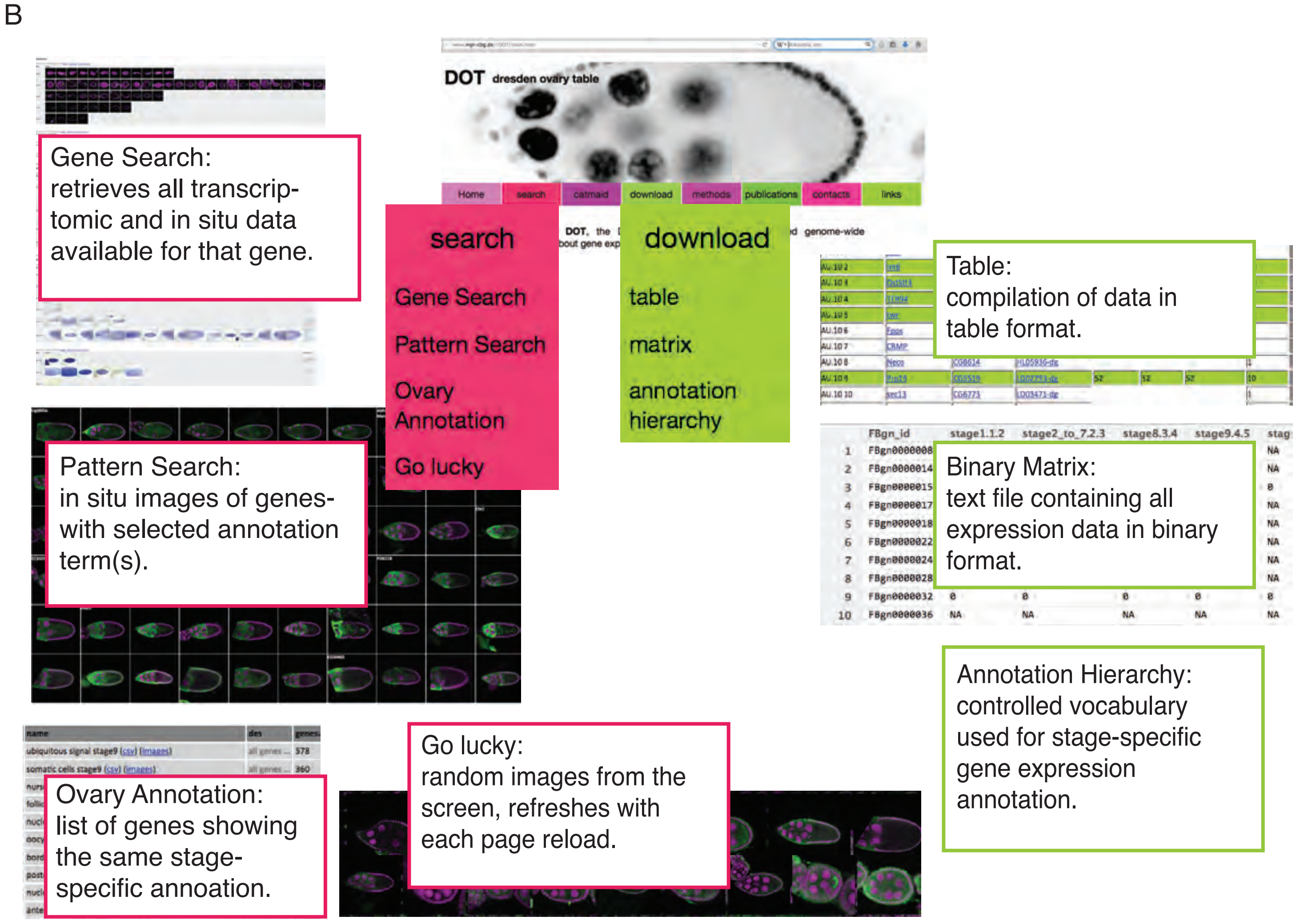
3A. Manual inspection of samples by wide-field microscopy.

3B. RNA extraction and mRNA enrichment.

4A. Automated aquisition and image processing of expression patterns.

4B. mRNA sequencing by RNAseq and 3Pseq.

5. Annotation and image upload to the database Dresden Ovary Table (DOT).



Gene Search: retrieves all transcriptomic and in situ data available for that gene.

Pattern Search: in situ images of genes with selected annotation term(s).

Ovary Annotation: list of genes showing the same stage-specific annoation.

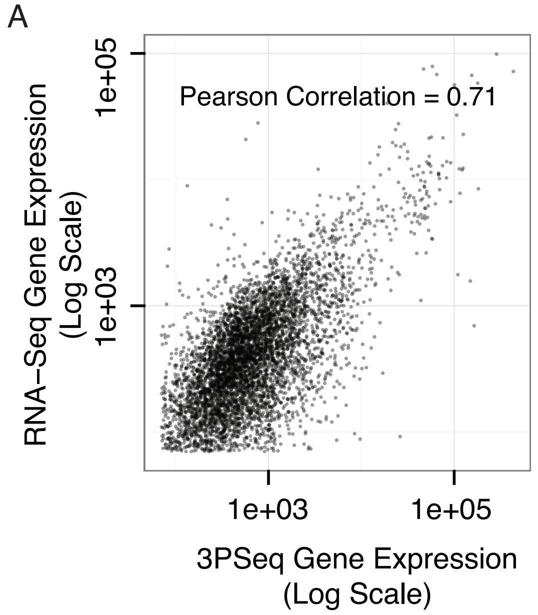
Go lucky: random images from the screen, refreshes with each page reload.

Table: compilation of data in table format.

Binary Matrix: text file containing all expression data in binary format.

Annotation Hierarchy: controlled vocabulary used for stage-specific gene expression annotation.

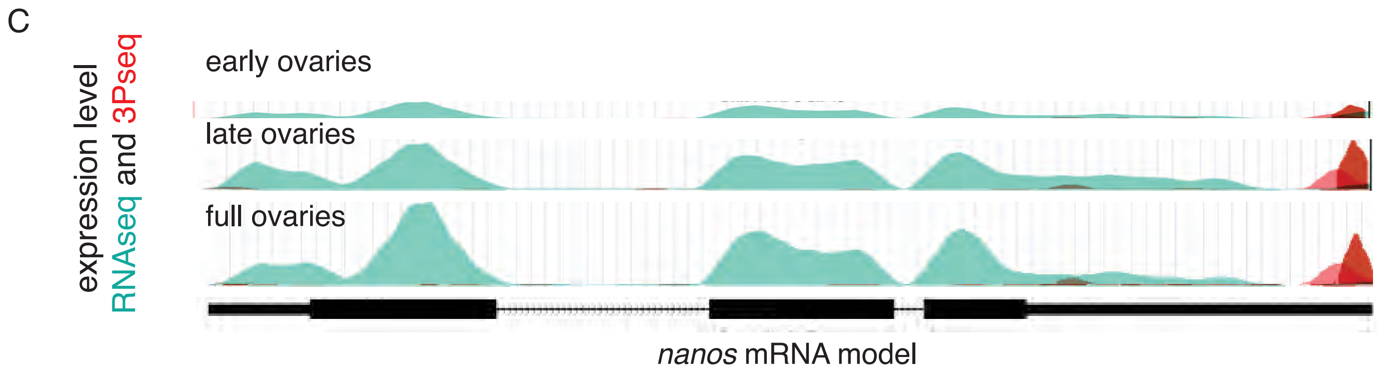
Figure S2



B

GO-term [BP] enrichment of UP/DOWN-regulated genes

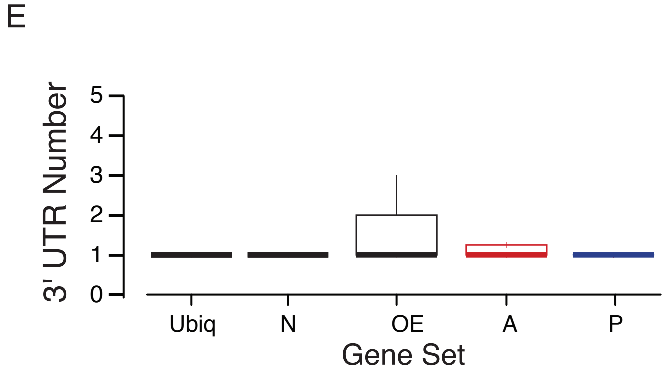
early DOWN	*Pval*	**early UP**	*Pval*
GO:0007423~sensory organ development	9.99E-08	GO:0008316~struct. const.vitelline membrane	1.11E-07
GO:0007548~sex differentiation	6.14E-07	**GO:0030704~vitelline membrane formation**	2.91E-06
GO:0001654~eye development	7.76E-07	GO:0007292~female gamete generation	6.33E-06
GO:0045137~development prim. sex. characteristics	1.08E-06	**GO:0030198~extracellular matrix organiz.**	1.55E-05
GO:0000122~negative regualtion of transcription	1.55E-05	**GO:0048609~reproductive process**	2.24E-05
GO:0003702~RNA Pol II transcritption factor activity	1.56E-04	GO:0005576~extracellular region	9.73E-05
GO:0030528~transcription regulator activity	1.90E-04	GO:0030703~eggshell formation	0.000274
GO:0051146~striated muscle cell development	3.63E-04	GO:0048477~oogenesis	0.0003
GO:0005604~basement	0.00167	GO:0005198~structural molecule activuty	0.000389
GO:0031012~extracellular amtrix	0.00248	**GO:0005811~lipid particle**	0.00039
late UP	*Pval*	**full DOWN**	*Pval*
GO:0042600~chorion	2.27E-23	GO:0042600~chorion	6.6824E-26
GO:0030312~external	1.06E-22	GO:0030312~external encapsulting structu	4.1567E-25
GO:0005576~extracellular	7.85E-09	GO:0010927~cellular component assembl	5.6186E-09
GO:0043292~contractile fiber	1E-07	GO:0007304~chorion-containing eggshell	9.3285E-09
GO:0019731~antibacterial humoral response	2.13E-07	GO:0005198~structural molecule activity	1.1953E-08
GO:0010927~cellular component assembly	2.61E-07	GO:0043292~contractile fiber	9.3649E-08
GO:0007304~chorion-containing assembly	4.09E-07	GO:0005576~extracellular region	3.4606E-07
GO:0030198~extracellular amtrix organization	3.22E-06	**GO:0030198~extracellular matrix organi**	1.6341E-06
GO:0007305~vitelline membrane formation	8.9E-06	GO:0030704~vitelline membrane formatio	5.159E-06
GO:0005198~structural molecule activity	1.14E-05	**GO:0030707~ovarian follicle cell**	7.817E-06
GO:0055114~oxidation reduction	2.92E-05	**GO:0005506~iron ion binding**	0.0002786



D

genes expressed as alternative isoforms

	early/late	late/full
oocyte-enriched	FBgn0002609 FBgn0004198 FBgn0030608 FBgn0040359	FBgn0030065 FBgn0030469 FBgn0033443
anterior	-	-
posterior	FBgn0004198 FBgn0016075	FBgn0033443



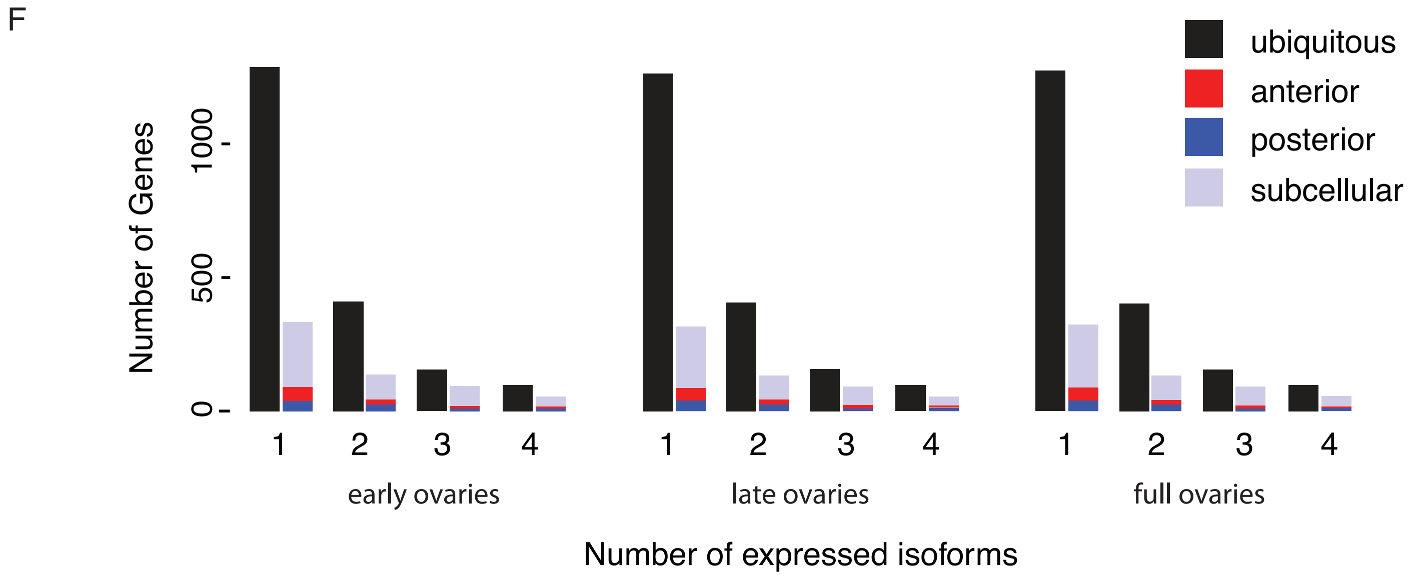


Figure S3

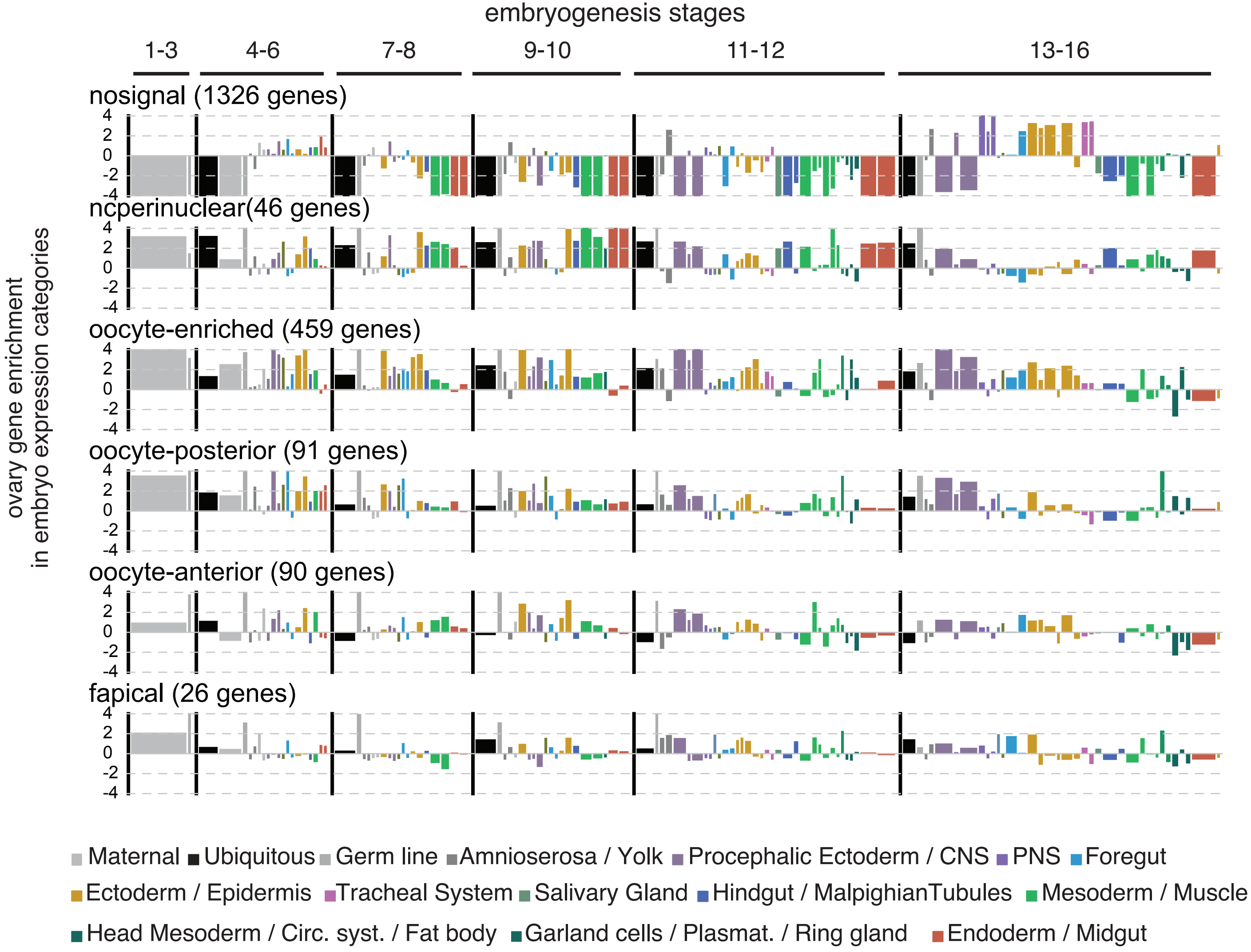
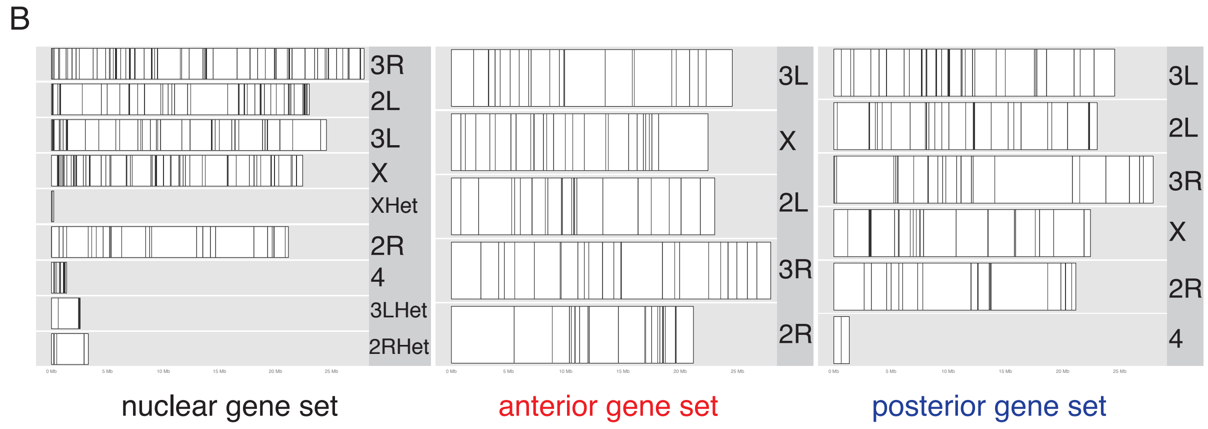
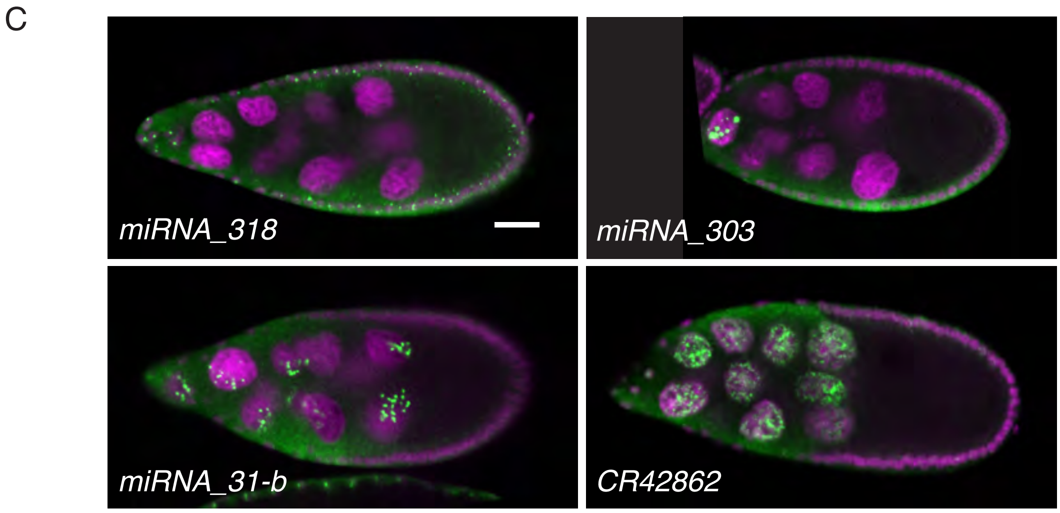

embryogenesis stages
1-3
4-6
7-8
9-10
11-12
13-16
ovary gene enrichment in embryo expression categories
nosignal (1326 genes)
ncperinuclear(46 genes)
oocyte-enriched (459 genes)
oocyte-posterior (91 genes)
oocyte-anterior (90 genes)
fapical (26 genes)
4
2
0
-2
-4
Maternal
Ubiquitous
Germ line
Amnioserosa / Yolk
Procephalic Ectoderm / CNS
PNS
Foregut
Ectoderm / Epidermis
Tracheal System
Salivary Gland
Hindgut / MalpighianTubules
Mesoderm / Muscle
Head Mesoderm / Circ. syst. / Fat body
Garland cells / Plasmat. / Ring gland
Endoderm / Midgut

Figure S4

A

	FISH: ubiq./ specifc signal	FISH: no signal
seq >= cutoff (early/late/full oogenesis	3021 (TP)	1111 (FN)
seq < cutoff (early/late/full oogenesis)	350 (FP)	890 (TN)





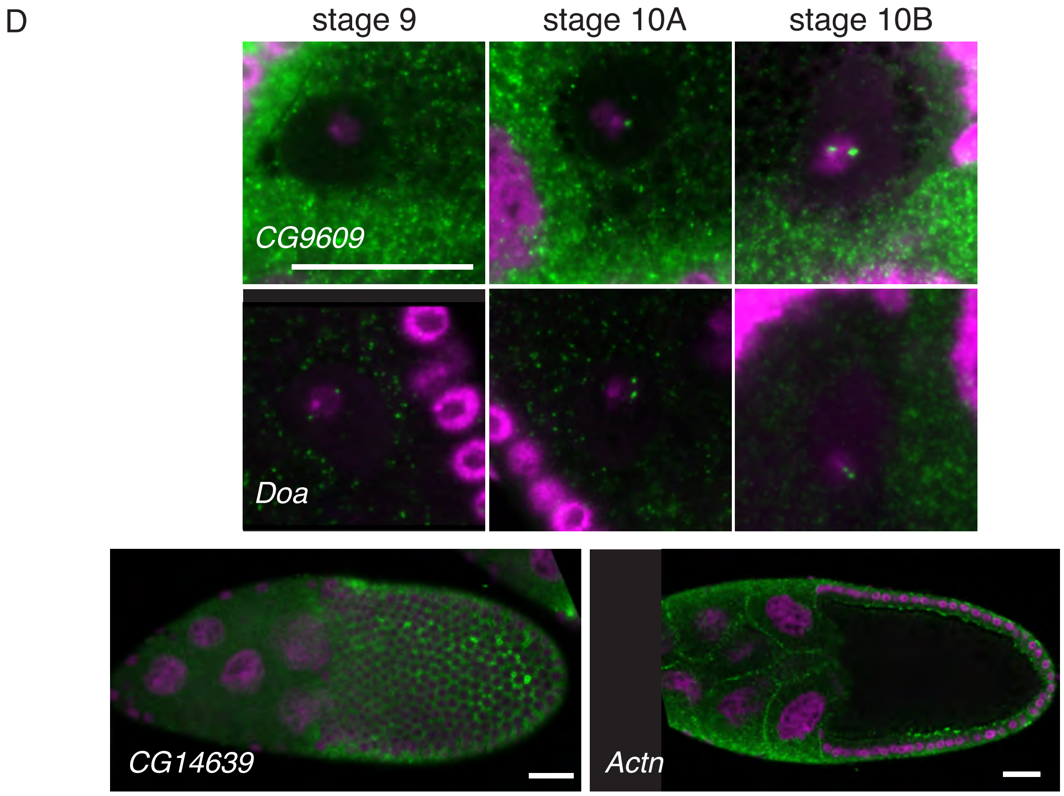


Figure S5

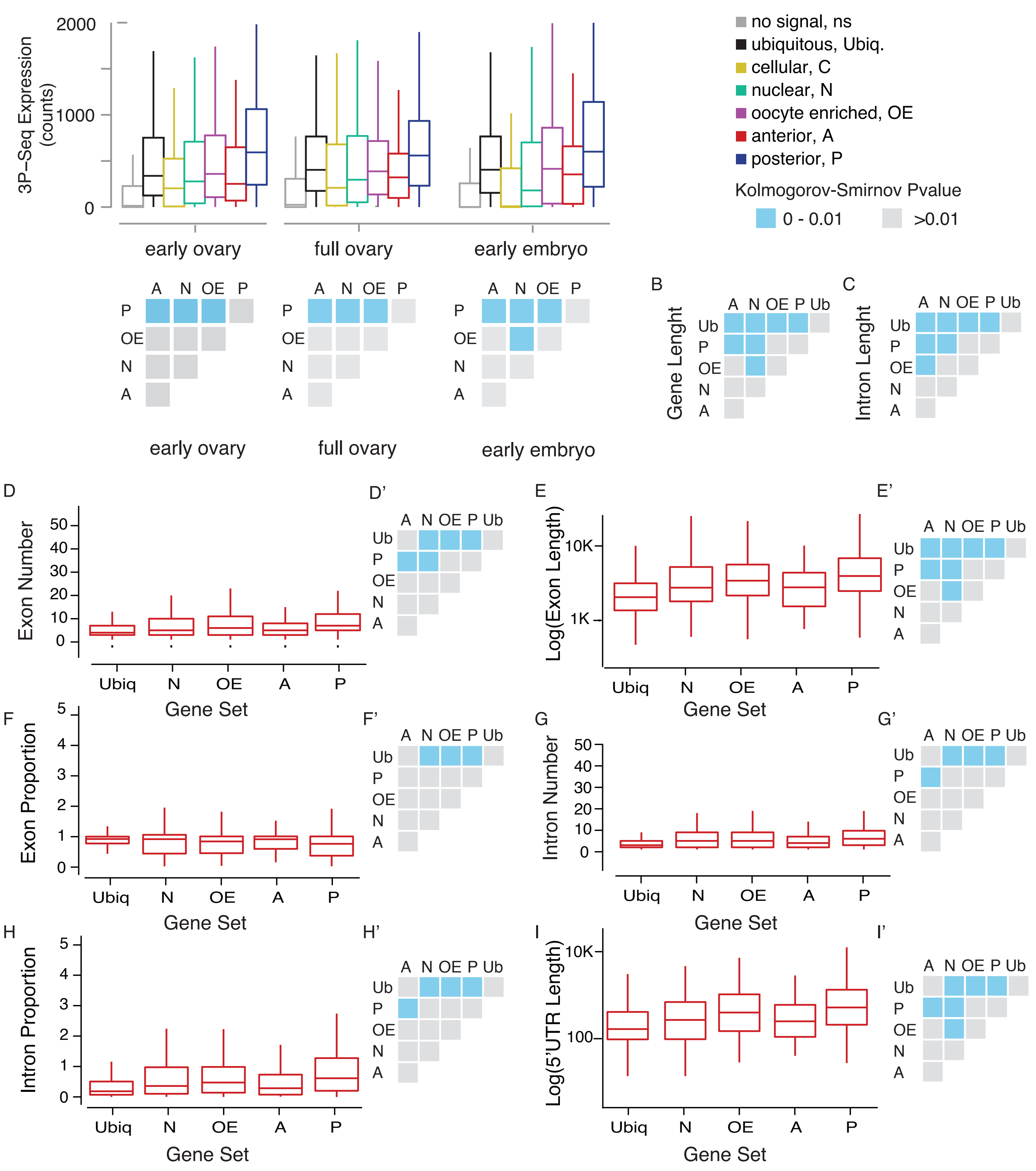

A
3P−Seq Expression (counts)
2000
1000
0
early ovary
full ovary
early embryo
no signal, ns
ubiquitous, Ubiq.
cellular, C
nuclear, N
oocyte enriched, OE
anterior, A
posterior, P
Kolmogorov-Smirnov Pvalue
0 - 0.01
>0.01
A N OE P
P
OE
N
A
early ovary
full ovary
early embryo
B
Gene Lenght
A N OE P Ub
Ub
P
OE
N
A
C
Intron Lenght
D
Exon Number
50
40
30
20
10
0
Ubiq N OE A P
Gene Set
D'
E
Log(Exon Length)
10K
1K
E'
F
Exon Proportion
5
4
3
2
1
0
F'
G
Intron Number
G'
H
Intron Proportion
H'
I
Log(5'UTR Length)
10K
100
I'

Figure S6

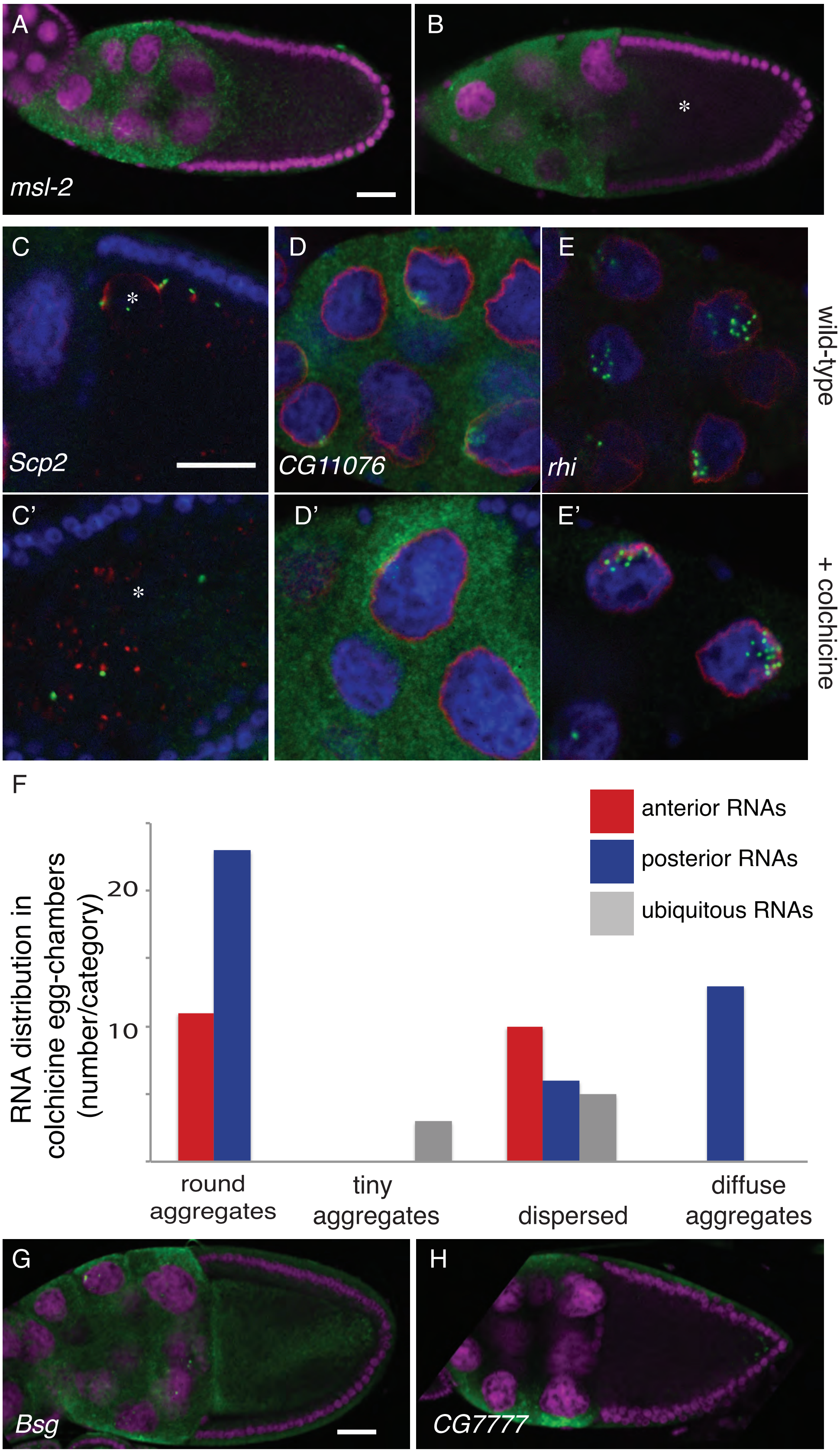
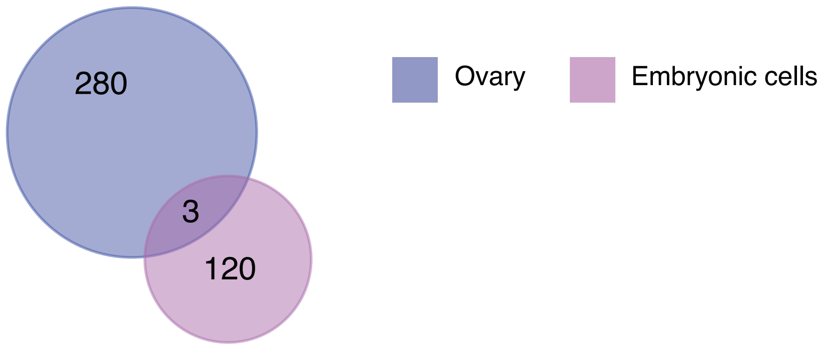

A
msl-2
B
*
C
*
Scp2
D
CG11076
E
rhi
wild-type
C'
*
D'
E'
+ colchicine
F
RNA distribution in colchicine egg-chambers (number/category)
20
10
anterior RNAs
posterior RNAs
ubiquitous RNAs
round aggregates
tiny aggregates
dispersed
diffuse aggregates
G
Bsg
H
CG7777

Figure S7

A

“localization-compentent” RNAs [BP]	P-value
GO:0007010~cytoskeleton organization	1.07E-14
GO:0045165~cell fate commitment	1.34E-12
GO:0001709~cell fate determination	1.99E-11
GO:0007552~metamorphosis	1.32E-10
GO:0007389~pattern specification process	2.23E-10
GO:0007017~microtubule-based process	2.64E-10
GO:0007444~imaginal disc development	2.76E-10
GO:0048707~instar larval or pupal morphogenesis	4.20E-10
GO:0009886~post-embryonic morphogenesis	4.47E-10

B



nuclear RNA enrichments

C